Enhancement of Calving Difficulty Breeding Values in New Zealand

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1. Introduction

A national genetic evaluation for the direct effect of calving difficulty (CD) in calves born to heifers was implemented in New Zealand (NZ) in the year 2000. Evaluations were done using a sire model (SM) that included relationships between sires and maternal grandsires, but no genetic grouping. Because AI bulls are mated to heifers far less frequently than to cows, a two-trait model, including CD in heifers (HCD) and CD in cows (CCD) was used to increase the accuracy of evaluation for HCD. The decision was made to move the genetic evaluation of CD to an animal model (AM). While doing so, a third trait, gestation length (GL), was included in the model so as to further increase the accuracy of evaluation. The purpose of this paper is to describe the new genetic evaluation system for HCD and to compare the breeding values (BVs) and reliabilities obtained from the SM and AM.

2. Materials and Methods

2.1. Variance Components

Variance components were estimated using the data from herds that participated in the original CD project. These herds were chosen because they were better recorded for CD than those in the wider population. Additionally, since the introduction of CD BV, the frequency that heifers were mated to difficult calving sires has reduced, thereby lowering the incidence of CD in calves born to heifers in recent years. The herds include LIC progeny test herds in season 1994, and progeny test herds from LIC and Ambreed, along with herds nominated by the NZ Holsetin Frieisan Association, in seasons 1995 and 1996. The data set contained 124,720 calving records, 15%, 33% and 52% collected in seasons 1994, 1995 and 1995, respectively. The breed composition of the calves was 58% Friesians, 19% Jerseys, 19% Friesian x Jersey Cross, <1% Ayrshires, 3% other crosses.

Because crossbreeding is common in NZ, breed of calf was defined as being Friesian, Jersey or Ayrshire, if it was at least 75% purebred. Friesian x Jersey Cross calves were at least 75% Friesian and Jersey. Approximately 10% of the records were collected from heifers. Fifty three percent of the calves were males.

CD was treated as a binary trait, either the calving was difficult or it was not difficult. While the degree of difficulty was recorded (in time taken to deliver the calf) there were so few records in some categories that all difficulties were treated as the same trait. The percentage of difficult calvings, by breed and sex of calf, and age of dam is shown in Table 1. Friesian calves experienced at least twice as much CD as calves of other breeds. More difficulty occurred in calves born from heifers than calves born from cows (approximately 10% versus 4% overall). Male calves experienced more CD than female calves. The incidence of CD in male and female calves born to heifers was approximately 13% and 7%, respectively. The corresponding incidence in calves born to cows was 5% and 3%, respectively.

Table 1. Percentage of difficult calvings by breed and sex of calf and age of dam.

	Heifers		Cows	
Calf Breed	M[1]	F[2]	M	F
Friesian	24.0	12.3	6.7	3.6
Jersey	3.9	2.6	1.2	1.1
FJ Cross	4.6	3.0	3.5	1.7
Ayrshire	10.9	2.1	1.5	0.9
Other X	8.2	7.5	3.6	1.9

[1] Male calves
[2] Female calves

GL was calculated for all calves in the data set using mating and calving dates on the national database. The average GL for male and female calves was 282.5 and 281.2

days, respectively, with a standard deviation around 4.2 days for both sexes.

Variance components were estimated using average information REML (Johnson & Thompson, 1995). A multiple-trait model that included HCD, CCD and GL was used. A sire model (sire/maternal grandsire pedigree) containing the effects of contemporary group (herd, season, age of dam as two years or greater than two years), sex of calf, breed fractions and heterozygosity, was used to analyse each trait.

2.2. National Data

The national data consisted of records from the research herds in seasons 1994 to 1996 and all herds in which recording was done from seasons 1997 to 2009. The dataset consisted of approximately 16 million records, with around 5% of the calvings coming from heifers. In seasons 1997 and later the average incidence of CD in calves born to heifers was 1.6% and 0.9% for male and females calves, respectively.

2.2. National Evaluation

The national evaluation was done using a multiple-trait AM for traits HCD, CCD and GL. For analysis and publication purposes, the binary CD traits are coded as 0 and 100. The genetic grouping strategy grouped animals with unknown parents by breed, country of origin and year of birth (Harris *et al.,* 1996). The fixed effects in the model included contemporary group, sex of calf and breed heterozygosity. Reliabilities were calculated using the method described by Harris and Johnson (1998).

3. Results and Discussion

3.1. Variance Components

Table 2 contains the estimates of the heritabilities and correlations of the CD and GL traits. The estimates associated with HCD and CCD are around one percentage point higher than those found in the original study. They are slightly lower than those found by others (McClintock, 2004; Jamrozik *et al.*, 2005; Olson *et al.*, 2009). The high positive genetic correlation between

HCD and CCD is of similar magnitude to that found by McClintock (2004) and indicates that using information on CCD would improve the reliability of sire BVs for HCD. The heritability of GL was moderately high and positively associated with CCD. The association of GL and HCD was close to zero. Hence, the impact of GL on the reliability of BVs for HCD would come primarily from the association with CCD.

Table 2. Estimates of the heritabilities and correlations of the CD traits and GL[1]

	HCD	CCD	GL
HCD	**0.045**	0.000	0.023
CCD	0.798	**0.030**	0.029
GL	0.024	0.197	**0.522**

[1]Heritabilities on diagonal, genetic correlations below diagonal, phenotypic correlations above diagonal.

3.2. National Evaluation

Comparisons of HCD BVs calculated from the SM and AM were done using sires that were born between 1990 and 2006 and had at least one progeny born from heifers. The data set consisted of 1750 Friesians, 2058 Jerseys and 454 Ayrshires (unlike the calves, these sires are essentially 100% purebred). The correlations between the BVs were 0.80, 0.66 and 0.75 for Friesians, Jerseys and Ayrshires, respectively. The correlation was lower for the Jersey than the other breeds because the progeny of Jersey sires experience CD far less frequently than the progeny of other breeds of sires. The addition of GL into the AM model allowed greater differentiation between sires and hence a reduced correlation between SM and AM BVs. Table 3 contains the standard deviations (SD) of the BVs from the two models. A reduction in the SD was evident for all breeds.

Table 3. Standard deviations of sire BVs for HCD obtained from the SM and AM.

Breed	Sire Model	Animal Model
Friesian	3.74	2.99
Jersey	1.54	1.19
Ayrshire	2.81	2.60

Table 4 contains the reliabilities of the BVs obtained from the two models. On average, there was a 17-point increase in reliabilities for the Jerseys and a 22-point increase for the other breeds when using the AM. The Friesians and Ayrshires had a slightly higher increase in reliability than the Jerseys because they had proportionally more progeny in the AM analysis than they had in the SM analysis.

Table 4. Reliabilities (%) of HCD BVs.

Breed	Sire Model	Animal Model
Friesian	49	71
Jersey	51	68
Ayrshire	42	64

In the AM, between 60% and 80% of the sires born in 1997 or later had their own record in the analysis. Comparisons were done between the change in HCD BV and associated reliability from the SM and AM of sires that did or did not have their own performance records in the data. There was no consistent difference between the change in HCD BV or reliabilities between the two groups of sires, indicating that the inclusion of the sire's own record in the analysis did not bias his genetic evaluation.

3.3. Genetic Trends

Figure 1 shows the annual genetic trends in HCD BVs obtained from the SM. The trends obtained from the AM are shown in Figure 2. The two models produced distinctly different trends. The SM shows a decreasing genetic trend in the HCD BVs of Friesian sires and an increasing trend in sires of the other two breeds. The trends were considerably smaller in the BVs obtained from the AM. Given that there is virtually no selection pressure for reduced HCD, the differences between the breed averages are expected to remain constant over time.
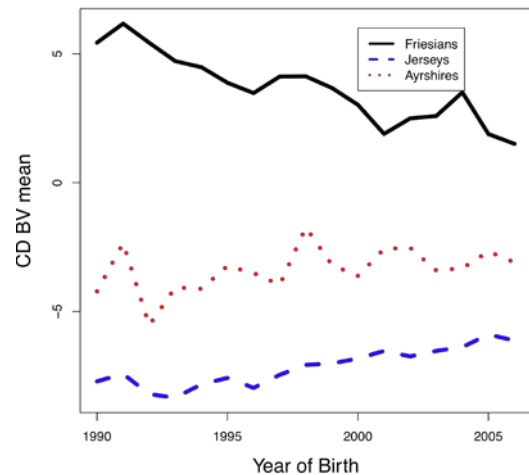

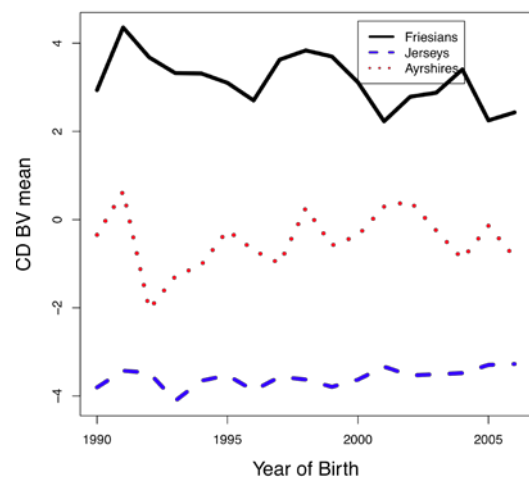**Figure 1.** Annual genetic trend in HCD BVs calculated using the SM.

Figure 2. Annual genetic trend in HCD BVs calculated using the AM.

Phenotypic trends were calculated by averaging the progeny means for HCD for Friesian and Jersey sires by year of birth. The difference between breed means, by year of birth, was calculated for the phenotypic data and for the HCD BVs obtained from the SM and AM. The trends are shown in Figure 3.
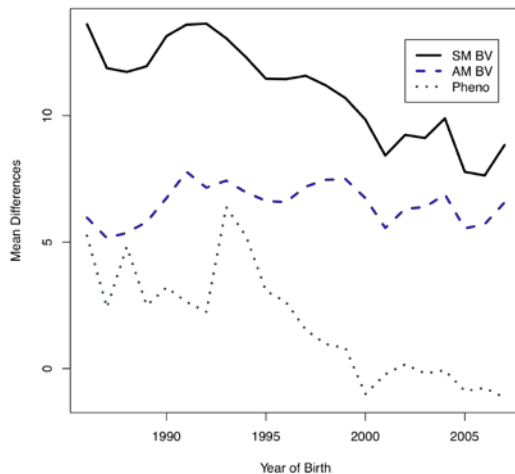

Figure 3. Differnces between Friesian and Jersey sires calculated using progeny phenotypic means, SM BVs and AM BVs for HCD.

The difference between the Friesian and Jersey HCD BVs calculated using an AM does not show a trend over time. The phenotypic difference between the breeds decreases over time, as does the difference calculated using the BVs obtained from the SM. The main differences between the SM and AM models were that the former did not contain genetic groups and did not account for the genetic merit of the dam. There is no selection on CD, but the Friesian and Jersey populations have different genetic merit. Crossbreeding between these breeds is common in NZ, and increasing over time. A SM does not take into account the effect of the specific sire-dam breed combination on the CD in their progeny. Progeny of a Friesian sire and Jersey dam would have a higher probability of experiencing CD than other sire-dam breed combinations. Reduced use of Friesian sires over Jersey dams over time would bias the sire genetic evaluations downwards over time unless the genetic merit of the dam was taken into account. Similarly, when there is potential of CD (for example heifers or small cows), there is a tendency to use Jersey sires instead of Friesian sires. Under this scenario, the progeny of Jersey sires would have a higher probability of CD than would the progeny arising from a more random use of these sires. Again, taking into account the genetic merit of the dam of the progeny would reduce the bias in sire evaluations. The results show that the use of a SM for the genetic evaluation of CD in NZ results in BVs that include environmental effects as well as genetic merit. The AM, on the other hand, results in a better separation of genetic and environmental trends.

4. Conclusions

This study shows that the evaluation of HCD using a multiple-trait AM that includes HCD, CCD and GL results in sires BVs that have higher reliability and less bias than those obtained from the SM.

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